



SEQUENCE LISTING

<110> Evans, Glen A.

<120> Nucleic Acids and Encoded Polypeptides
Associated with Bipolar Disorder

<130> P-EA 4672

<140> US 09/922,225

<141> 2001-08-02

<160> 117

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<221> CDS

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Ala Ser Ser Gly Asp Thr Ala Pro Ala Ala Asp Lys Leu Arg Glu Leu
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ctg ggc agc cga gag gcg ggc ggc gcg gag cac cgg acc gag tta tct 147
Leu Gly Ser Arg Glu Ala Gly Gly Ala Glu His Arg Thr Glu Leu Ser
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ggg aac aaa gca gga caa gtc tgg gca cct gaa gga tct act gct ttc 195
Gly Asn Lys Ala Gly Gln Val Trp Ala Pro Glu Gly Ser Thr Ala Phe
50 55 60

aag tgt ctg ctt tca gca agg tta tgt gct gct ctc ctg agc aac atc 243
Lys Cys Leu Leu Ser Ala Arg Leu Cys Ala Ala Leu Leu Ser Asn Ile
65 70 75

tct gac tgt gat gaa aca ttc aac tac tgg gag cca aca cac tac ctc 291
Ser Asp Cys Asp Glu Thr Phe Asn Tyr Trp Glu Pro Thr His Tyr Leu
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Ile Tyr Gly Glu Gly Phe Gln Thr Trp Glu Tyr Ser Pro Ala Tyr Ala
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cat gca aga att cta caa act aat aag att ctt gtg ttt tac ttt ttg	435
His Ala Arg Ile Leu Gln Thr Asn Lys Ile Leu Val Phe Tyr Phe Leu	
130 135 140	
cga tgt ctt ctg gct ttt gtg agc tgt att tgt gaa ctt tac ttt tac	483
Arg Cys Leu Leu Ala Phe Val Ser Cys Ile Cys Glu Leu Tyr Phe Tyr	
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Lys Ala Val Cys Lys Lys Phe Gly Leu His Val Ser Arg Met Met Leu	
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Ala Phe Leu Val Leu Ser Thr Gly Met Phe Cys Ser Ser Ser Ala Phe	
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ctt cct agt agc ttc tgt atg tac act acg ttg ata gcc atg act gga	627
Leu Pro Ser Ser Phe Cys Met Tyr Thr Thr Leu Ile Ala Met Thr Gly	
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Trp Tyr Met Asp Lys Thr Ser Ile Ala Val Leu Gly Val Ala Ala Gly	
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Ser Leu Met Ala Leu Ile Leu Phe Leu Val Pro Val Val Val Ile Asp	
255 260 265 270	
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Ser Tyr Tyr Tyr Gly Lys Leu Val Ile Ala Pro Leu Asn Ile Val Leu	
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Tyr Asn Val Phe Thr Pro His Gly Pro Asp Leu Tyr Gly Thr Glu Pro	
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Trp Tyr Phe Tyr Leu Ile Asn Gly Phe Leu Asn Phe Asn Val Ala Phe	
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gct ttg gct ctc cta gtc cta cca ctg act tct ctt atg gaa tac ctg	1011
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al
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 Gly Ala Val Ala Leu Ser Ala Leu Gln Lys Cys Tyr His Phe Val Phe
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 415 420 425 430

gca ctg ttc aga gga tat cac ggg ccc ctt gat ttg tat cca gaa ttt 1347
 Ala Leu Phe Arg Gly Tyr His Gly Pro Leu Asp Leu Tyr Pro Glu Phe
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tac cga att gct aca gac cca acc atc cac act gtc cca gaa ggc aga 1395
 Tyr Arg Ile Ala Thr Asp Pro Thr Ile His Thr Val Pro Glu Gly Arg
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cct gtg aat gtc tgt gtg gga aaa gag tgg tat cga ttt ccc agc agc 1443
 Pro Val Asn Val Cys Val Gly Lys Glu Trp Tyr Arg Phe Pro Ser Ser
 465 470 475

ttc ctt ctt cct gac aat tgg cag ctt cag ttc att cca tca gag ttc 1491
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aga ggt cag tta cca aaa cct ttt gca gaa gga cct ctg gcc acc cgg 1539
 Arg Gly Gln Leu Pro Lys Pro Phe Ala Glu Gly Pro Leu Ala Thr Arg
 495 500 505 510

att gtt cct act gac atg aat gac cag aat cta gaa gag cca tcc aga 1587
 Ile Val Pro Thr Asp Met Asn Asp Gln Asn Leu Glu Glu Pro Ser Arg
 515 520 525

tat att gat atc agt aaa tgc cat tat tta gtg gat ttg gac acc atg 1635
 Tyr Ile Asp Ile Ser Lys Cys His Tyr Leu Val Asp Leu Asp Thr Met
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 560 565 570

ctg ctg cgg gca ttc tat gtc ccc ttc ctg tca gat cag tat aca gtg 1779
 Leu Leu Arg Ala Phe Tyr Val Pro Phe Leu Ser Asp Gln Tyr Thr Val
 575 580 585 590

tac gta aac tac acc atc ctc aaa ccc cgg aaa gca aag caa atc agg 1827
 Tyr Val Asn Tyr Thr Ile Leu Lys Pro Arg Lys Ala Lys Gln Ile Arg
 595 600 605

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 Lys Lys Ser Gly Gly
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 35 40 45
 Lys Ala Gly Gln Val Trp Ala Pro Glu Gly Ser Thr Ala Phe Lys Cys
 50 55 60
 Leu Leu Ser Ala Arg Leu Cys Ala Ala Leu Leu Ser Asn Ile Ser Asp
 65 70 75 80
 Cys Asp Glu Thr Phe Asn Tyr Trp Glu Pro Thr His Tyr Leu Ile Tyr
 85 90 95
 Gly Glu Gly Phe Gln Thr Trp Glu Tyr Ser Pro Ala Tyr Ala Ile Arg
 100 105 110
 Ser Tyr Ala Tyr Leu Leu Leu His Ala Trp Pro Ala Ala Phe His Ala
 115 120 125
 Arg Ile Leu Gln Thr Asn Lys Ile Leu Val Phe Tyr Phe Leu Arg Cys
 130 135 140
 Leu Leu Ala Phe Val Ser Cys Ile Cys Glu Leu Tyr Phe Tyr Lys Ala
 145 150 155 160
 Val Cys Lys Lys Phe Gly Leu His Val Ser Arg Met Met Leu Ala Phe
 165 170 175
 Leu Val Leu Ser Thr Gly Met Phe Cys Ser Ser Ser Ala Phe Leu Pro
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 Met Asp Lys Thr Ser Ile Ala Val Leu Gly Val Ala Ala Gly Ala Ile

a!
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	260	265
Tyr Tyr Gly Lys Leu Val Ile Ala Pro Leu Asn Ile Val Leu Tyr Asn		270
	275	280
Val Phe Thr Pro His Gly Pro Asp Leu Tyr Gly Thr Glu Pro Trp Tyr		285
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Phe Tyr Leu Ile Asn Gly Phe Leu Asn Phe Asn Val Ala Phe Ala Leu		300
305	310	315
Ala Leu Leu Val Leu Pro Leu Thr Ser Leu Met Glu Tyr Leu Leu Gln		320
	325	330
Arg Phe His Val Gln Asn Leu Gly His Pro Tyr Trp Leu Thr Leu Ala		335
	340	345
Pro Met Tyr Ile Trp Phe Ile Ile Phe Phe Ile Gln Pro His Lys Glu		350
	355	360
Glu Arg Phe Leu Phe Pro Val Tyr Pro Leu Ile Cys Leu Cys Gly Ala		365
	370	375
Val Ala Leu Ser Ala Leu Gln Lys Cys Tyr His Phe Val Phe Gln Arg		380
385	390	395
Tyr Arg Leu Glu His Tyr Thr Val Thr Ser Asn Trp Leu Ala Leu Gly		400
	405	410
Thr Val Phe Leu Phe Gly Leu Leu Ser Phe Ser Arg Ser Val Ala Leu		415
	420	425
Phe Arg Gly Tyr His Gly Pro Leu Asp Leu Tyr Pro Glu Phe Tyr Arg		430
	435	440
Ile Ala Thr Asp Pro Thr Ile His Thr Val Pro Glu Gly Arg Pro Val		445
	450	455
Asn Val Cys Val Gly Lys Glu Trp Tyr Arg Phe Pro Ser Ser Phe Leu		460
465	470	475
Leu Pro Asp Asn Trp Gln Leu Gln Phe Ile Pro Ser Glu Phe Arg Gly		480
	485	490
Gln Leu Pro Lys Pro Phe Ala Glu Gly Pro Leu Ala Thr Arg Ile Val		495
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Pro Thr Asp Met Asn Asp Gln Asn Leu Glu Glu Pro Ser Arg Tyr Ile		510
	515	520
Asp Ile Ser Lys Cys His Tyr Leu Val Asp Leu Asp Thr Met Arg Glu		525
	530	535
Thr Pro Arg Glu Pro Lys Tyr Ser Ser Asn Lys Glu Glu Trp Ile Ser		540
545	550	555
Leu Ala Tyr Arg Pro Phe Leu Asp Ala Ser Arg Ser Ser Lys Leu Leu		560
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Arg Ala Phe Tyr Val Pro Phe Leu Ser Asp Gln Tyr Thr Val Tyr Val		575
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Met Thr
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gag tgg gac cct gtg cca cag agt gag acc ctg tct caa aaa aaa aaa 166
Glu Trp Asp Pro Val Pro Gln Ser Glu Thr Leu Ser Gln Lys Lys Lys
5 10 15

cta tgt aaa tcc aag gag acg act tca cct gta ttg tac ctc tcc aag 214
Leu Cys Lys Ser Lys Glu Thr Thr Ser Pro Val Leu Tyr Leu Ser Lys
20 25 30

ttc tgg aaa gtc gat gga ggg ttt act cag aac ttc aat cta tcc aga 262
Phe Trp Lys Val Asp Gly Gly Phe Thr Gln Asn Phe Asn Leu Ser Arg
35 40 45 50

act gag ttt tgt tta tgg tgt gtg cca gtt cag aat tta ggc cac ccg 310
Thr Glu Phe Cys Leu Trp Cys Val Pro Val Gln Asn Leu Gly His Pro
55 60 65

tat tgg ctt acc ttg gct cca atg tat att tgg ttt ata att ttc ttc 358
Tyr Trp Leu Thr Leu Ala Pro Met Tyr Ile Trp Phe Ile Ile Phe Phe
70 75 80

atc cag cct cac aaa gag gag aga ttt ctt ttc cct gtg tat cca ctt 406
Ile Gln Pro His Lys Glu Glu Arg Phe Leu Phe Pro Val Tyr Pro Leu
85 90 95

ata tgt ctc tgt ggc gct gtg gct ctc tct gca ctt cag aaa tgt tac 454
Ile Cys Leu Cys Gly Ala Val Ala Leu Ser Ala Leu Gln Lys Cys Tyr
100 105 110

cac ttt gtg ttt caa cga tat cgc ctg gag cac tat act gtg aca tcg 502
His Phe Val Phe Gln Arg Tyr Arg Leu Glu His Tyr Thr Val Thr Ser
115 120 125 130

aat tgg ctg gca tta gga act gtc ttc ctg ttt ggg ctc ttg tca ttt 550
Asn Trp Leu Ala Leu Gly Thr Val Phe Leu Phe Gly Leu Leu Ser Phe
135 140 145

tct cgc tct gtg gca ctg ttc aga gga tat cac ggg ccc ctt gat ttg 598
Ser Arg Ser Val Ala Leu Phe Arg Gly Tyr His Gly Pro Leu Asp Leu
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tat cca gaa ttt tac cga att gct aca gac cca acc atc cac act gtc 646
Tyr Pro Glu Phe Tyr Arg Ile Ala Thr Asp Pro Thr Ile His Thr Val

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Pro Glu Gly Arg Pro Val Asn Val Cys Val Gly Lys Glu Trp Tyr Arg			
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Phe Pro Ser Ser Phe Leu Leu Pro Asp Asn Trp Gln Leu Gln Phe Ile			
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cca tca gag ttc aga ggt cag tta cca aaa cct ttt gca gaa gga cct			790
Pro Ser Glu Phe Arg Gly Gln Leu Pro Lys Pro Phe Ala Glu Gly Pro			
215	220	225	
ctg gcc acc cgg att gtt cct act gac atg aat gac cag aat cag aag			838
Leu Ala Thr Arg Ile Val Pro Thr Asp Met Asn Asp Gln Asn Gln Lys			
230	235	240	
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35 40 45	
Ser Arg Thr Glu Phe Cys Leu Trp Cys Val Pro Val Gln Asn Leu Gly	
50 55 60	
His Pro Tyr Trp Leu Thr Leu Ala Pro Met Tyr Ile Trp Phe Ile Ile	
65 70 75 80	
Phe Phe Ile Gln Pro His Lys Glu Glu Arg Phe Leu Phe Pro Val Tyr	
85 90 95	
Pro Leu Ile Cys Leu Cys Gly Ala Val Ala Leu Ser Ala Leu Gln Lys	
100 105 110	
Cys Tyr His Phe Val Phe Gln Arg Tyr Arg Leu Glu His Tyr Thr Val	
115 120 125	
Thr Ser Asn Trp Leu Ala Leu Gly Thr Val Phe Leu Phe Gly Leu Leu	
130 135 140	
Ser Phe Ser Arg Ser Val Ala Leu Phe Arg Gly Tyr His Gly Pro Leu	
145 150 155 160	
Asp Leu Tyr Pro Glu Phe Tyr Arg Ile Ala Thr Asp Pro Thr Ile His	
165 170 175	
Thr Val Pro Glu Gly Arg Pro Val Asn Val Cys Val Gly Lys Glu Trp	
180 185 190	
Tyr Arg Phe Pro Ser Ser Phe Leu Leu Pro Asp Asn Trp Gln Leu Gln	
195 200 205	

Phe	Ile	Pro	Ser	Glu	Phe	Arg	Gly	Gln	Leu	Pro	Lys	Pro	Phe	Ala	Glu
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Gly	Pro	Leu	Ala	Thr	Arg	Ile	Val	Pro	Thr	Asp	Met	Asn	Asp	Gln	Asn
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Gln	Lys	Ser	His	Pro	Asp	Ile	Leu	Ile	Ser	Val	Asn	Ala	Ile	Ile	
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					1	

aca	gag	tgg	gac	cct	gtg	cca	cag	agt	gag	acc	ctg	tct	caa	aaa	aaa	164
Thr	Glu	Trp	Asp	Pro	Val	Pro	Gln	Ser	Glu	Thr	Leu	Ser	Gln	Lys	Lys	
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Lys	Leu	Cys	Lys	Ser	Lys	Glu	Thr	Thr	Ser	Pro	Val	Leu	Tyr	Leu	Ser	
		20					25					30				

aag	ttc	tgg	aaa	gtc	gat	gga	ggg	ttt	act	cag	aac	ttc	aat	cta	tcc	260
Lys	Phe	Trp	Lys	Val	Asp	Gly	Gly	Phe	Thr	Gln	Asn	Phe	Asn	Leu	Ser	
		35				40					45					

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Arg	Thr	Glu	Phe	Cys	Leu	Trp	Cys	Val	Pro	Val	Gln	Asn	Leu	Gly	His	
	50				55				60						65	

ccg	tat	tgg	ctt	acc	ttg	gct	cca	atg	tat	att	tgg	ttt	ata	att	ttc	356
Pro	Tyr	Trp	Leu	Thr	Leu	Ala	Pro	Met	Tyr	Ile	Trp	Phe	Ile	Ile	Phe	
				70					75						80	

ttc	atc	cag	cct	cac	aaa	gag	gag	aga	ttt	ctt	ttc	cct	gtg	tat	cca	404
Phe	Ile	Gln	Pro	His	Lys	Glu	Glu	Arg	Phe	Leu	Phe	Pro	Val	Tyr	Pro	
			85					90					95			

ctt	ata	tgt	ctc	tgt	ggc	gct	gtg	gct	ctc	tct	gca	ctt	cag	aaa	tgt	452
Leu	Ile	Cys	Leu	Cys	Gly	Ala	Val	Ala	Leu	Ser	Ala	Leu	Gln	Lys	Cys	
		100					105					110				

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Tyr	His	Phe	Val	Phe	Gln	Arg	Tyr	Arg	Leu	Glu	His	Tyr	Thr	Val	Thr	
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Phe Ser Arg Ser Val Ala Leu Phe Arg Gly Tyr His Gly Pro Leu Asp	
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ttg tat cca gaa ttt tac cga att gct aca gac cca acc atc cac act	644
Leu Tyr Pro Glu Phe Tyr Arg Ile Ala Thr Asp Pro Thr Ile His Thr	
165 170 175	
gtc cca gaa ggc aga cct gtg aat gtc tgt gtg gga aaa gag tgg tat	692
Val Pro Glu Gly Arg Pro Val Asn Val Cys Val Gly Lys Glu Trp Tyr	
180 185 190	
cga ttt ccc agc agc ttc ctt ctt cct gac aat tgg cag ctt cag ttc	740
Arg Phe Pro Ser Ser Phe Leu Leu Pro Asp Asn Trp Gln Leu Gln Phe	
195 200 205	
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Ile Pro Ser Glu Phe Arg Gly Gln Leu Pro Lys Pro Phe Ala Glu Gly	
210 215 220 225	
cct ctg gcc acc cgg att gtt cct act gac atg aat gac cag aat cta	836
Pro Leu Ala Thr Arg Ile Val Pro Thr Asp Met Asn Asp Gln Asn Leu	
230 235 240	
gaa gag cca tcc aga tat att gat atc agt aaa tgc cat tat tta gtg	884
Glu Glu Pro Ser Arg Tyr Ile Asp Ile Ser Lys Cys His Tyr Leu Val	
245 250 255	
gat ttg gac acc atg aga gaa aca ccc cgg gag cca aaa tat tca tcc	932
Asp Leu Asp Thr Met Arg Glu Thr Pro Arg Glu Pro Lys Tyr Ser Ser	
260 265 270	
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Asn Lys Glu Glu Trp Ile Ser Leu Ala Tyr Arg Pro Phe Leu Asp Ala	
275 280 285	
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Ser Arg Ser Ser Lys Leu Leu Arg Ala Phe Tyr Val Pro Phe Leu Ser	
290 295 300 305	
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Asp Gln Tyr Thr Val Tyr Val Asn Tyr Thr Ile Leu Lys Pro Arg Lys	
310 315 320	
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Ala Lys Gln Ile Arg Lys Lys Ser Gly Gly	
325 330	
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 35 40 45
 Ser Arg Thr Glu Phe Cys Leu Trp Cys Val Pro Val Gln Asn Leu Gly
 50 55 60
 His Pro Tyr Trp Leu Thr Leu Ala Pro Met Tyr Ile Trp Phe Ile Ile
 65 70 75 80
 Phe Phe Ile Gln Pro His Lys Glu Glu Arg Phe Leu Phe Pro Val Tyr
 85 90 95
 Pro Leu Ile Cys Leu Cys Gly Ala Val Ala Leu Ser Ala Leu Gln Lys
 100 105 110
 Cys Tyr His Phe Val Phe Gln Arg Tyr Arg Leu Glu His Tyr Thr Val
 115 120 125
 Thr Ser Asn Trp Leu Ala Leu Gly Thr Val Phe Leu Phe Gly Leu Leu
 130 135 140
 Ser Phe Ser Arg Ser Val Ala Leu Phe Arg Gly Tyr His Gly Pro Leu
 145 150 155 160
 Asp Leu Tyr Pro Glu Phe Tyr Arg Ile Ala Thr Asp Pro Thr Ile His
 165 170 175
 Thr Val Pro Glu Gly Arg Pro Val Asn Val Cys Val Gly Lys Glu Trp
 180 185 190
 Tyr Arg Phe Pro Ser Ser Phe Leu Leu Pro Asp Asn Trp Gln Leu Gln
 195 200 205
 Phe Ile Pro Ser Glu Phe Arg Gly Gln Leu Pro Lys Pro Phe Ala Glu
 210 215 220
 Gly Pro Leu Ala Thr Arg Ile Val Pro Thr Asp Met Asn Asp Gln Asn
 225 230 235 240
 Leu Glu Glu Pro Ser Arg Tyr Ile Asp Ile Ser Lys Cys His Tyr Leu
 245 250 255
 Val Asp Leu Asp Thr Met Arg Glu Thr Pro Arg Glu Pro Lys Tyr Ser
 260 265 270
 Ser Asn Lys Glu Glu Trp Ile Ser Leu Ala Tyr Arg Pro Phe Leu Asp
 275 280 285
 Ala Ser Arg Ser Ser Lys Leu Leu Arg Ala Phe Tyr Val Pro Phe Leu
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<222> (1)...(1017)

<400> 7

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Met Ala Ser Arg Gly Ala Arg Gln Arg Leu Lys Gly Ser Gly Ala Ser
1 5 10 15

agt ggg gat acg gcc ccg gct gcg gac aag ctg cgg gag ctg ctg ggc 96
Ser Gly Asp Thr Ala Pro Ala Ala Asp Lys Leu Arg Glu Leu Leu Gly
20 25 30

agc cga gag gcg ggc ggc gcg gag cac cgg acc gag tta tct ggg aac 144
Ser Arg Glu Ala Gly Gly Ala Glu His Arg Thr Glu Leu Ser Gly Asn
35 40 45

aaa gca gga caa gtc tgg gca cct gaa gga tct act gct ttc aag tgt 192
Lys Ala Gly Gln Val Trp Ala Pro Glu Gly Ser Thr Ala Phe Lys Cys
50 55 60

ctg ctt tca gca agg tta tgt gct gct ctc ctg agc aac atc tct gac 240
Leu Leu Ser Ala Arg Leu Cys Ala Ala Leu Leu Ser Asn Ile Ser Asp
65 70 75 80

tgt gat gaa aca ttc aac tac tgg gag cca aca cac tac ctc atc tat 288
Cys Asp Glu Thr Phe Asn Tyr Trp Glu Pro Thr His Tyr Leu Ile Tyr
85 90 95

ggg gaa ggg ttt cag act tgg gaa tat tcc cca gca tat gcc att cgc 336
Gly Glu Gly Phe Gln Thr Trp Glu Tyr Ser Pro Ala Tyr Ala Ile Arg
100 105 110

tcc tat gct tac ctg ttg ctt cat gcc tgg cca gct gca ttt cat gca 384
Ser Tyr Ala Tyr Leu Leu Leu His Ala Trp Pro Ala Ala Phe His Ala
115 120 125

aga att cta caa act aat aag att ctt gtg ttt tac ttt ttg cga tgt 432
Arg Ile Leu Gln Thr Asn Lys Ile Leu Val Phe Tyr Phe Leu Arg Cys
130 135 140

ctt ctg gct ttt gtg agc tgt att tgt gaa ctt tac ttt tac aag gct 480
Leu Leu Ala Phe Val Ser Cys Ile Cys Glu Leu Tyr Phe Tyr Lys Ala
145 150 155 160

gtg tgc aag aag ttt ggg ttg cac gtg agt cga atg atg cta gcc ttc 528
Val Cys Lys Lys Phe Gly Leu His Val Ser Arg Met Met Leu Ala Phe
165 170 175

ttg gtt ctc agc act ggc atg ttt tgc tca tca tca gca ttc ctt cct 576
Leu Val Leu Ser Thr Gly Met Phe Cys Ser Ser Ser Ala Phe Leu Pro
180 185 190

agt agc ttc tgt atg tac act acg ttg ata gcc atg act gga tgg tat 624
Ser Ser Phe Cys Met Tyr Thr Thr Leu Ile Ala Met Thr Gly Trp Tyr

195	200	205	
atg gac aag act tcc att gct gtg ctg gga gta gca gct ggg gct atc			672
Met Asp Lys Thr Ser Ile Ala Val Leu Gly Val Ala Ala Gly Ala Ile			
210	215	220	
tta ggc tgg cca ttc agt gca gct ctt ggt tta ccc att gcc ttt gat			720
Leu Gly Trp Pro Phe Ser Ala Ala Leu Gly Leu Pro Ile Ala Phe Asp			
225	230	235	240
ttg ctg gtc atg aaa cac agg tgg aag agt ttc ttt cat tgg tcg ctg			768
Leu Leu Val Met Lys His Arg Trp Lys Ser Phe Phe His Trp Ser Leu			
	245	250	255
atg gcc ctc ata cta ttt ctg gtg cct gtg gtg gtc att gac agc tac			816
Met Ala Leu Ile Leu Phe Leu Val Pro Val Val Val Ile Asp Ser Tyr			
	260	265	270
tat tat ggg aag ttg gtg att gca cca ctc aac att gtt ttg tat aat			864
Tyr Tyr Gly Lys Leu Val Ile Ala Pro Leu Asn Ile Val Leu Tyr Asn			
	275	280	285
gtc ttt act cct cat gga cct gat ctt tat ggt aca gaa ccc tgg tat			912
Val Phe Thr Pro His Gly Pro Asp Leu Tyr Gly Thr Glu Pro Trp Tyr			
	290	295	300
ttc tat tta att aat gga ttt ctg aat ttc aat gta gcc ttt gct ttg			960
Phe Tyr Leu Ile Asn Gly Phe Leu Asn Phe Asn Val Ala Phe Ala Leu			
305	310	315	320
gct ctc cta gtc cta cca ctg act tct ctt atg gaa tac ctg ctg cag			1008
Ala Leu Leu Val Leu Pro Leu Thr Ser Leu Met Glu Tyr Leu Leu Gln			
	325	330	335
aga ttt cat			1017
Arg Phe His			

<210> 8
 <211> 339
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Ala Ser Arg Gly Ala Arg Gln Arg Leu Lys Gly Ser Gly Ala Ser
 1 5 10 15
 Ser Gly Asp Thr Ala Pro Ala Ala Asp Lys Leu Arg Glu Leu Leu Gly
 20 25 30
 Ser Arg Glu Ala Gly Gly Ala Glu His Arg Thr Glu Leu Ser Gly Asn
 35 40 45
 Lys Ala Gly Gln Val Trp Ala Pro Glu Gly Ser Thr Ala Phe Lys Cys
 50 55 60
 Leu Leu Ser Ala Arg Leu Cys Ala Ala Leu Leu Ser Asn Ile Ser Asp
 65 70 75 80

Cys Asp Glu Thr Phe Asn Tyr Trp Glu Pro Thr His Tyr Leu Ile Tyr
 85 90 95
 Gly Glu Gly Phe Gln Thr Trp Glu Tyr Ser Pro Ala Tyr Ala Ile Arg
 100 105 110
 Ser Tyr Ala Tyr Leu Leu Leu His Ala Trp Pro Ala Ala Phe His Ala
 115 120 125
 Arg Ile Leu Gln Thr Asn Lys Ile Leu Val Phe Tyr Phe Leu Arg Cys
 130 135 140
 Leu Leu Ala Phe Val Ser Cys Ile Cys Glu Leu Tyr Phe Tyr Lys Ala
 145 150 155 160
 Val Cys Lys Lys Phe Gly Leu His Val Ser Arg Met Met Leu Ala Phe
 165 170 175
 Leu Val Leu Ser Thr Gly Met Phe Cys Ser Ser Ser Ala Phe Leu Pro
 180 185 190
 Ser Ser Phe Cys Met Tyr Thr Thr Leu Ile Ala Met Thr Gly Trp Tyr
 195 200 205
 Met Asp Lys Thr Ser Ile Ala Val Leu Gly Val Ala Ala Gly Ala Ile
 210 215 220
 Leu Gly Trp Pro Phe Ser Ala Ala Leu Gly Leu Pro Ile Ala Phe Asp
 225 230 235 240
 Leu Leu Val Met Lys His Arg Trp Lys Ser Phe Phe His Trp Ser Leu
 245 250 255
 Met Ala Leu Ile Leu Phe Leu Val Pro Val Val Val Ile Asp Ser Tyr
 260 265 270
 Tyr Tyr Gly Lys Leu Val Ile Ala Pro Leu Asn Ile Val Leu Tyr Asn
 275 280 285
 Val Phe Thr Pro His Gly Pro Asp Leu Tyr Gly Thr Glu Pro Trp Tyr
 290 295 300
 Phe Tyr Leu Ile Asn Gly Phe Leu Asn Phe Asn Val Ala Phe Ala Leu
 305 310 315 320
 Ala Leu Leu Val Leu Pro Leu Thr Ser Leu Met Glu Tyr Leu Leu Gln
 325 330 335
 Arg Phe His

<210> 9
 <211> 556
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (150)...(554)

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 ggcattccagt ggttcaaggt tacaataagc tgtgatcgtg ccactgcatt ctacctggga 120
 tgacagagtg ggacctgtg ccacagagt gag acc ctg tct caa aaa aaa aaa 173
 Glu Thr Leu Ser Gln Lys Lys Lys
 1 5
 aaa cta tgt aaa tcc aag aaa aaa aga aaa cag ctc ctg tgg cct ttt 221
 Lys Leu Cys Lys Ser Lys Lys Lys Arg Lys Gln Leu Leu Trp Pro Phe
 10 15 20

gcc tct cat cca gaa agg gta tcc att ggc ctt tct aat atc tct tca	269
Ala Ser His Pro Glu Arg Val Ser Ile Gly Leu Ser Asn Ile Ser Ser	
25 30 35 40	
tcc tgt cag gcc aca aat gga gac gac cca cct gta tgg tac ctc tcc	317
Ser Cys Gln Ala Thr Asn Gly Asp Asp Pro Pro Val Trp Tyr Leu Ser	
45 50 55	
aag ttc tgg aaa gtc gat gga ggg ttt act cag aac ttc aat cta tcc	365
Lys Phe Trp Lys Val Asp Gly Gly Phe Thr Gln Asn Phe Asn Leu Ser	
60 65 70	
aga act gag ttt ggt aaa tgg tgt gtg cca ggc agg gga tta aac agt	413
Arg Thr Glu Phe Gly Lys Trp Cys Val Pro Gly Arg Gly Leu Asn Ser	
75 80 85	
agt gca tat cac tgg gct gaa gtg aca gga att caa gaa cag aat gca	461
Ser Ala Tyr His Trp Ala Glu Val Thr Gly Ile Gln Glu Gln Asn Ala	
90 95 100	
tcc act cct cca gtc tca tta agc tgc ctc ttt cta ctg aaa tgg cga	509
Ser Thr Pro Pro Val Ser Leu Ser Cys Leu Phe Leu Leu Lys Trp Arg	
105 110 115 120	
tgg gga ttc cag gac acc tct caa cct aca gga acc act gga tct	554
Trp Gly Phe Gln Asp Thr Ser Gln Pro Thr Gly Thr Thr Gly Ser	
125 130 135	
aa	556

<210> 10
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 10

Glu Thr Leu Ser Gln Lys Lys Lys Lys Leu Cys Lys Ser Lys Lys Lys	
1 5 10 15	
Arg Lys Gln Leu Leu Trp Pro Phe Ala Ser His Pro Glu Arg Val Ser	
20 25 30	
Ile Gly Leu Ser Asn Ile Ser Ser Ser Cys Gln Ala Thr Asn Gly Asp	
35 40 45	
Asp Pro Pro Val Trp Tyr Leu Ser Lys Phe Trp Lys Val Asp Gly Gly	
50 55 60	
Phe Thr Gln Asn Phe Asn Leu Ser Arg Thr Glu Phe Gly Lys Trp Cys	
65 70 75 80	
Val Pro Gly Arg Gly Leu Asn Ser Ser Ala Tyr His Trp Ala Glu Val	
85 90 95	
Thr Gly Ile Gln Glu Gln Asn Ala Ser Thr Pro Pro Val Ser Leu Ser	
100 105 110	
Cys Leu Phe Leu Leu Lys Trp Arg Trp Gly Phe Gln Asp Thr Ser Gln	
115 120 125	
Pro Thr Gly Thr Thr Gly Ser	
130 135	

<210> 11
 <211> 577
 <212> PRT
 <213> S. cerevisiae

<400> 11
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 1 5 10 15
 Thr Phe Ser Ile Leu Ala Val Leu Arg Leu Thr Ser Ala Ser Phe Arg
 20 25 30
 Val Ile Asp Asp Cys Asp Glu Val Tyr Asn Tyr Trp Glu Pro Leu His
 35 40 45
 Tyr Leu Leu Tyr Gly Tyr Gly Leu Gln Thr Trp Glu Tyr Ser Pro Glu
 50 55 60
 Tyr Ala Ile Arg Ser Trp Phe Tyr Ile Ala Leu His Ala Val Pro Gly
 65 70 75 80
 Phe Leu Ala Arg Gly Leu Gly Leu Ser Arg Leu His Val Phe Tyr Phe
 85 90 95
 Ile Arg Gly Val Leu Ala Cys Phe Ser Ala Phe Cys Glu Thr Asn Leu
 100 105 110
 Ile Leu Ala Val Ala Arg Asn Phe Asn Arg Ala Val Ala Leu His Leu
 115 120 125
 Thr Ser Val Leu Phe Val Asn Ser Gly Met Trp Ser Ala Ser Thr Ser
 130 135 140
 Phe Leu Pro Ser Ser Phe Ala Met Asn Met Val Thr Leu Ala Leu Ser
 145 150 155 160
 Ala Gln Leu Ser Pro Pro Ser Thr Lys Arg Thr Val Lys Val Val Ser
 165 170 175
 Phe Ile Thr Ile Gly Ala Val Ile Gly Trp Pro Phe Ser Ala Ala Leu
 180 185 190
 Ser Ile Pro Phe Ile Leu Leu Glu Leu Val Asp Leu Lys Gly Arg Phe
 195 200 205
 Arg His Leu Phe Cys Arg Trp Phe Lys Ala Ile Phe Val Ala Leu Leu
 210 215 220
 Ile Thr Gly Ile Cys Ile Thr Val Asp Ser Leu Phe Tyr His Arg Ile
 225 230 235 240
 Gln Phe Val Ala Trp Asn Ile Val Lys Tyr Asn Val Leu Ala Lys Asp
 245 250 255
 Gly Arg Gly Pro Asp Ile Tyr Gly Thr Glu Pro Trp Trp Tyr Tyr Phe
 260 265 270
 Ala Asn Leu Ser Leu Gln His Asn Ile Val Leu Trp Phe Ala Met Ala
 275 280 285
 Cys Gly Pro Leu Val Leu Leu Ala Ala Phe Thr Asn Trp Ile Asn Leu
 290 295 300
 Asp Ser Phe Leu Asp Leu Ser Ser Val Ile Ser Pro Phe Tyr Ile Trp
 305 310 315 320
 Leu Phe Ile Phe Ile Gln Pro His Lys Glu Glu Arg Phe Met Tyr
 325 330 335
 Pro Ile Tyr Pro Val Leu Cys Leu Ala Ala Ala Ile Gly Leu Asp Met
 340 345 350
 Ser Leu Lys Leu Met Ile Gln Ile Leu Ser Ser Ile Asn Glu Thr Val
 355 360 365
 Arg Ser Lys Phe Pro Val Arg Phe Val Val Leu Cys Val Tyr Ala Ile

a!
 cont

370		375		380
Ile Gly Cys Leu Ser	Ile Ala Arg Ile Leu	Ala Ile Gln Asn Tyr Asn		
385	390	395	400	
Ala Pro Met Ile Ile	Tyr Pro Ala Ile Ser	Phe Leu Glu Thr Asp Asn		
	405	410	415	
Asn Val Thr Thr	Asn Val Cys Val Gly	Lys Glu Trp Tyr Arg Tyr Pro		
	420	425	430	
Ser Thr Phe Phe	Leu Pro Asp Asn Ser Arg	Leu Lys Phe Val Lys Ser		
	435	440	445	
Glu Phe Asp Gly	Ile Leu Pro Gly Glu Phe	Val Glu Ser Asn Ser Thr		
	450	455	460	
Trp Trp Asn Arg	Glu Gly Tyr Tyr Gln Ile	Pro Glu His Met Asn Glu		
465	470	475	480	
Phe Asn Asn Glu	Glu Pro Thr Arg Tyr Thr	Ser Leu Glu Ser Cys Asp		
	485	490	495	
Phe Leu Ile Asp	Leu Glu Phe Asp His Ser	Lys Ala Thr Val Asn Glu		
	500	505	510	
Pro Ile Tyr Ser	Lys Ser Asp Gly Trp Ile	Pro Val Met Val Tyr Pro		
	515	520	525	
Phe Ile Asp Thr	Lys Gln Thr Pro Phe Met	Gly Arg Ala Phe Ala Val		
	530	535	540	
Pro Phe Ile Glu	Pro Lys Trp Gly Arg Tyr	Glu Ile Leu Val Lys Lys		
545	550	555	560	
Pro Val Lys Ile	Asp Phe Ser Asn Leu Arg	Ala Ser Lys Gln Gln		
	565	570	575	

Ala

<210> 12
 <211> 570
 <212> PRT
 <213> A. thalania

a!
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Met Asp Leu Thr Thr Thr Arg Gln Arg Arg Pro Leu Ile Ser Asp Ser
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Ser Ser Ser Ser Thr Lys Ser Tyr Ser Lys Thr Asp Lys Pro Gly
20 25 30
Arg Ser Asn Gly Gly Asp Ala Glu Asp Gly Gly Leu Arg Trp Phe Leu
35 40 45
Pro Phe Ile Ala Leu Cys Tyr Leu Arg Tyr Met Ser Ala Thr Ser Asn
50 55 60
Ile Ile His Asp Cys Asp Glu Val Phe Asn Tyr Trp Glu Pro Leu His
65 70 75 80
Tyr Ile Leu Tyr Lys Ser Gly Phe Gln Thr Trp Glu Tyr Ser Ser Asn
85 90 95
Phe Ala Leu Arg Ser Tyr Leu Tyr Ile Leu Phe His Glu Leu Ala Gly
100 105 110
Arg Pro Ala Ser Trp Trp Phe Gly Asp Asp Lys Val Arg Val Phe Tyr
115 120 125
Ala Val Arg Leu Phe Leu Gly Leu Val Ser Ala Val Ser Asp Thr Val
130 135 140
Leu Val Val Ala Leu Ser Arg Lys Tyr Gly Lys Arg Ile Ala Thr Tyr
145 150 155 160

Ala Val Ala Met Leu Cys Leu Thr Ser Gly Cys Phe Phe Ala Ser Thr
165 170 175
Ser Phe Leu Pro Ser Ser Phe Ser Met Tyr Ala Ile Ser Leu Ser Ser
180 185 190
Gly Leu Leu Leu Phe Glu Lys Tyr Ala Met Ala Val Ala Val Ser Val
195 200 205
Val Gly Val Ile Leu Gly Trp Pro Phe Ser Ile Leu Ala Phe Leu Pro
210 215 220
Val Val Ile Tyr Ser Leu Val Lys Arg Phe Lys Gln Ala Phe Ile Ala
225 230 235 240
Gly Ala Val Thr Thr Ile Phe Leu Leu Gly Val Ser Leu Leu Val Asp
245 250 255
Tyr Tyr Tyr Tyr Lys Arg Trp Thr Ser Ser Val Leu Asn Leu Leu Ile
260 265 270
Tyr Asn Val Leu Gly Gly Gly Glu Ser His Leu Tyr Gly Thr Glu Gly
275 280 285
Ala Leu Phe Tyr Ile Arg Asn Gly Phe Asn Asn Phe Asn Phe Cys Phe
290 295 300
Ile Leu Ala Met Leu Phe Val Ala Ile Tyr Pro Val Ile Arg Arg Lys
305 310 315 320
Tyr Asp Arg Ala Leu Val Val Ile Ser Pro Met Tyr Ile Trp Leu
325 330 335
Ala Phe Met Ser Leu Gln Pro His Lys Glu Glu Arg Phe Leu Tyr Pro
340 345 350
Ile Tyr Pro Leu Ile Cys Val Ser Ala Ser Ala Val Ile Glu Asn Ile
355 360 365
Pro Glu Leu Phe Arg Glu Lys Tyr Ser Ser Arg Glu Ser Leu Leu Val
370 375 380
Thr Ile Thr Lys Tyr Met Arg Pro Val Ile Leu Gly Cys Ile Leu Cys
385 390 395 400
Ala Ser His Ser Arg Thr Phe Ala Leu Ile Asn Gly Tyr Ser Ala Pro
405 410 415
Leu Glu Val Tyr Lys Leu Leu Glu His His Asp Asp Ala Gly Pro Gly
420 425 430
Ser Val Leu Cys Val Gly Ser Glu Trp His Arg Tyr Pro Ser Ser Phe
435 440 445
Phe Val Pro His Tyr Ile Ser Glu Val Arg Trp Ile Asp Asp Gly Phe
450 455 460
Arg Gly Leu Leu Pro Phe Pro Phe Asn Asn Thr Leu Gly Gly Thr Ser
465 470 475 480
Ala Ser Pro Pro Tyr Phe Asn Asn Lys Asn Gln Ala Ser Glu Glu Gln
485 490 495
Tyr Leu Lys Asn Ile Glu Thr Cys Thr Phe Leu Ile Glu Leu Gln Leu
500 505 510
Ser Arg Pro Tyr Gln Tyr Arg Gly Ser Asp Leu Ser Thr Trp Glu Ala
515 520 525
Ile Ala Val Leu Pro Tyr Leu Asp Arg Glu Leu Ser Pro Ala Lys Tyr
530 535 540
Arg Ser Phe Phe Ile Pro His Met Trp Gln Glu Lys Asn Val Phe Gly
545 550 555 560
Lys Tyr Val Ala Leu Arg Arg Val Pro Lys
565 570

<210> 13

<211> 653
 <212> PRT
 <213> C. elegans

<400> 13

Met	Val	Thr	His	Arg	Arg	Lys	Gly	Gly	Ser	Gly	Pro	Pro	Gln	Lys	Pro
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Pro	Pro	Arg	Ile	Val	Asp	Arg	Ser	Ser	Phe	Asp	Ala	Asp	Lys	Lys	Lys
		20					25						30		
Ile	Lys	Val	Glu	Lys	Leu	Tyr	His	Lys	Ala	Asn	Asn	Pro	Asp	Asn	Asp
	35					40						45			
Trp	Pro	Phe	Ser	Phe	Gly	Ser	Val	Phe	Lys	Met	Leu	Leu	Ser	Ile	Arg
	50				55					60					
Ile	Ser	Gly	Ala	Ile	Trp	Gly	Ile	Ile	Asn	Asp	Cys	Asp	Glu	Val	Tyr
65				70					75					80	
Asn	Tyr	Trp	Glu	Pro	Leu	His	Leu	Phe	Leu	Tyr	Gly	Glu	Gly	Phe	Gln
			85					90						95	
Thr	Trp	Glu	Tyr	Ser	Pro	Val	Tyr	Ala	Ile	Arg	Ser	Tyr	Phe	Tyr	Ile
		100						105					110		
Tyr	Leu	His	Tyr	Ile	Pro	Ala	Ser	Leu	Phe	Ala	Asn	Leu	Phe	Gly	Asp
	115						120					125			
Thr	Lys	Ile	Val	Val	Phe	Thr	Leu	Ile	Arg	Leu	Thr	Ile	Gly	Leu	Phe
	130					135				140					
Cys	Leu	Leu	Gly	Glu	Tyr	Ala	Phe	Asp	Ala	Ile	Cys	Lys	Lys	Lys	Ile
145				150				155						160	
Asn	Ile	Ala	Thr	Gly	Arg	Phe	Phe	Ile	Leu	Phe	Ser	Ile	Phe	Ser	Ser
			165					170					175		
Gly	Met	Phe	Leu	Ala	Ser	Thr	Ala	Phe	Val	Pro	Ser	Ser	Phe	Cys	Met
		180					185						190		
Ala	Ile	Thr	Phe	Tyr	Ile	Leu	Gly	Ala	Tyr	Leu	Asn	Glu	Asn	Trp	Thr
	195						200					205			
Ala	Gly	Ile	Phe	Cys	Val	Ala	Phe	Ser	Thr	Met	Val	Gly	Trp	Pro	Phe
	210					215					220				
Ser	Ala	Val	Leu	Gly	Leu	Pro	Ile	Val	Ala	Asp	Met	Leu	Leu	Leu	Lys
225				230						235					240
Gly	Leu	Arg	Ile	Arg	Phe	Ile	Leu	Thr	Ser	Leu	Val	Ile	Gly	Leu	Cys
			245					250					255		
Ile	Gly	Gly	Val	Gln	Val	Ile	Thr	Asp	Ser	His	Tyr	Phe	Gly	Lys	Thr
		260					265						270		
Val	Leu	Ala	Pro	Leu	Asn	Ile	Phe	Leu	Tyr	Asn	Val	Val	Ser	Gly	Pro
	275						280					285			
Gly	Pro	Ser	Leu	Tyr	Gly	Glu	Glu	Pro	Leu	Ser	Phe	Tyr	Ile	Lys	Asn
	290					295					300				
Leu	Phe	Asn	Asn	Trp	Asn	Ile	Val	Ile	Phe	Ala	Ala	Pro	Phe	Gly	Phe
305				310						315					320
Pro	Leu	Ser	Leu	Ala	Tyr	Phe	Thr	Lys	Val	Trp	Met	Ser	Gln	Asp	Arg
			325					330					335		
Asn	Val	Ala	Leu	Tyr	Gln	Arg	Phe	Ala	Pro	Ile	Ile	Leu	Leu	Ala	Val
		340						345					350		
Thr	Thr	Ala	Ala	Trp	Leu	Leu	Ile	Phe	Gly	Ser	Gln	Ala	His	Lys	Glu
	355						360					365			
Glu	Arg	Phe	Leu	Phe	Pro	Ile	Tyr	Pro	Phe	Ile	Ala	Phe	Phe	Ala	Ala
	370					375					380				
Leu	Ala	Leu	Asp	Ala	Thr	Asn	Arg	Leu	Cys	Leu	Lys	Lys	Leu	Gly	Met
385				390						395					400

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cont

Asp	Asn	Ile	Leu	Ser	Ile	Leu	Phe	Ile	Leu	Cys	Phe	Ala	Ile	Leu	Ser	405	410	415
Ala	Ser	Arg	Thr	Tyr	Ser	Ile	His	Asn	Asn	Tyr	Gly	Ser	His	Val	Glu	420	425	430
Ile	Tyr	Arg	Ser	Leu	Asn	Ala	Glu	Leu	Thr	Asn	Arg	Thr	Asn	Phe	Lys	435	440	445
Asn	Phe	His	Asp	Pro	Ile	Arg	Val	Cys	Val	Gly	Lys	Glu	Trp	His	Arg	450	455	460
Phe	Pro	Ser	Ser	Phe	Phe	Ile	Pro	Gln	Thr	Val	Ser	Asp	Gly	Lys	Lys	465	470	475
Val	Glu	Met	Arg	Phe	Ile	Gln	Ser	Glu	Phe	Arg	Gly	Leu	Leu	Pro	Lys	485	490	495
Pro	Phe	Leu	Lys	Ser	Asp	Lys	Leu	Val	Glu	Val	Thr	Arg	His	Ile	Pro	500	505	510
Thr	Glu	Met	Asn	Asn	Leu	Asn	Gln	Glu	Glu	Ile	Ser	Arg	Tyr	Val	Asp	515	520	525
Leu	Asp	Ser	Cys	Asp	Tyr	Val	Val	Asp	Val	Asp	Met	Pro	Gln	Ser	Asp	530	535	540
Arg	Glu	Pro	Asp	Phe	Arg	Lys	Met	Arg	Gln	Asn	Tyr	Lys	Arg	Lys	Thr	545	550	555
Lys	Lys	Lys	Trp	Lys	Arg	Ile	Glu	Asn	Ala	Ile	Leu	Gln	Phe	Trp	Leu	565	570	575
Asn	Ser	Leu	Phe	Glu	Glu	Ile	Lys	Phe	Leu	Asn	Ser	Asn	Phe	His	Ser	580	585	590
Phe	Pro	Phe	Phe	Val	Phe	Asp	Asn	Phe	Gly	Leu	Phe	Gln	Ala	Tyr		595	600	605
Ser	His	Tyr	Ser	Phe	Leu	Lys	Ile	Thr	Gly	Asn	Gln	Trp	Ile	Arg	Phe	610	615	620
His	Ser	Ser	Met	Ser	Pro	Asn	Gln	Gln	Asp	Ser	Met	Gly	Phe	Phe	Val	625	630	635
His	Phe	Met	Phe	His	Ser	Phe	Leu	Pro	Asn	Ile	Met	Ser				645	650	

<210> 14
 <211> 623
 <212> PRT
 <213> D. melangaster

<400> 14

Met	Ala	Pro	Pro	Ala	Ala	Arg	Ala	Arg	Tyr	Ile	Ala	Asn	Lys	Ala	Asp	1	5	10	15
Asn	Gln	Ile	Leu	Ser	Lys	Lys	Pro	Pro	Lys	Arg	Pro	Gly	Leu	Asn	Gly	20	25	30	
Asn	Asn	Lys	Thr	Lys	Glu	Ala	Thr	Pro	Ala	Gly	Lys	Lys	Lys	Asp	Lys	35	40	45	
Asp	Ala	Lys	Lys	Arg	Asn	Gln	Pro	Thr	Ser	Gly	Gly	Gln	Glu	Lys	Gly	50	55	60	
Leu	Pro	Asn	Pro	Ile	Met	Pro	Ser	Val	Gln	Thr	Ala	Phe	Lys	Thr	Phe	65	70	75	80
Val	Ser	Ala	Arg	Leu	Cys	Ser	Ala	Ile	Trp	Ala	Tyr	Ile	Ala	Asp	Cys	85	90	95	
Asp	Glu	Thr	Phe	Asn	Tyr	Trp	Glu	Pro	Leu	His	Tyr	Ile	Ile	Asn	Gly	100	105	110	
His	Gly	Leu	Gln	Thr	Trp	Glu	Tyr	Ser	Pro	Gln	Phe	Gly	Leu	Arg	Ser				

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cont

Tyr	Thr	Ala	Leu	Glu	Pro	Asn	Tyr	Ser	Lys	Arg	Ser	Lys	Asp	Trp	Ser
				565					570					575	
Val	Met	Lys	Ser	Leu	Pro	Phe	Leu	Ile	Pro	Glu	Lys	Ser	His	Lys	Val
				580				585					590		
Leu	Arg	Ala	Phe	Tyr	Val	Pro	Phe	Leu	Thr	Asp	Asn	His	Ile	Gln	Tyr
				595				600				605			
Gly	Asp	Phe	Asn	Leu	Leu	Lys	Arg	Lys	Thr	Lys	Arg	Asn	Gly	Arg	
	610						615				620				

<210> 15
 <211> 577
 <212> PRT
 <213> S. pombe

<400> 15

Met	Pro	Ser	Lys	Ala	Pro	Arg	Lys	Ser	Leu	Ser	Val	Ser	Phe	Val	Trp
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Thr	Phe	Ser	Ile	Leu	Ala	Val	Leu	Arg	Leu	Thr	Ser	Ala	Ser	Phe	Arg
				20				25					30		
Val	Ile	Asp	Asp	Cys	Asp	Glu	Val	Tyr	Asn	Tyr	Trp	Glu	Pro	Leu	His
		35					40					45			
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				85				90					95		
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Arg	His	Leu	Phe	Cys	Arg	Trp	Phe	Lys	Ala	Ile	Phe	Val	Ala	Leu	Leu
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Gln	Phe	Val	Ala	Trp	Asn	Ile	Val	Lys	Tyr	Asn	Val	Leu	Ala	Lys	Asp
				245				250						255	
Gly	Arg	Gly	Pro	Asp	Ile	Tyr	Gly	Thr	Glu	Pro	Trp	Trp	Tyr	Tyr	Phe
			260				265						270		
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		275					280					285			
Cys	Gly	Pro	Leu	Val	Leu	Leu	Ala	Ala	Phe	Thr	Asn	Trp	Ile	Asn	Leu
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